

GenCore version 5.1.4.P5.4578  
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## OM protein - protein search, using sw model

Run on: May 12, 2003, 15:00:12; Search time 50 Seconds  
(without alignments)  
1520.847 Million cell updates/sec

Title: US-09-804-472-2

Perfect score: 4177  
Sequence: 1 MASSDPYLPYDGGGDNPL.....DILRHMAQTANQDPASIMFN 791Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database:

1: PIR.73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4026	96.4	820	2	I37240	chloride channel F
2	3996	95.7	760	2	S55473	chloride channel F
3	3994	95.6	760	2	I58159	protein kinase C-1
4	3273	78.4	760	2	I37242	chloride channel F
5	3240	77.6	747	2	S47327	chloride channel F
6	3217	77.0	747	2	I48294	chloride channel F
7	2100.5	50.3	735	2	T19065	gene Clcn4 protein
8	1086	26.0	260	2	I37277	probable protein F
9	1020.5	24.4	772	2	T02805	chloride channel F
10	1015	24.3	812	2	T39817	chloride channel F
11	999.5	23.9	779	2	S50054	hypothetical prote
12	773	18.5	810	2	T24009	hypothetical prote
13	751.5	18.0	802	2	S68426	hypothetical prote
14	750.5	18.0	789	2	S68427	chloride channel F
15	725.5	17.4	869	2	S68428	chloride channel F
16	724.5	17.3	800	2	T01843	probable chloride
17	709	17.0	667	2	T40727	chloride channel F
18	684.5	16.4	764	2	T07608	probable chloride
19	671.5	16.1	780	2	T02939	chloride channel F
20	670.5	16.1	775	2	T52107	chloride channel F
21	657.5	15.7	902	2	T16821	anion channel prote
22	652	15.6	907	2	S23399	hypothetical prote
23	649	15.5	950	2	T15815	hypothetical prote
24	646	15.5	822	2	S68210	hypothetical prote
25	635.5	15.2	887	2	T25358	hypothetical prote
26	624.5	15.0	880	2	T18771	probable chloride
27	602.5	14.4	994	2	S19595	chloride channel F
28	591	14.1	810	2	S19725	voltage-gated chor
29	590.5	14.1	805	2	S13410	chloride channel F

30	579.5	13.9	988	2	S37078	chloride channel p
31	534	12.8	687	2	A57713	chloride channel C
32	530.5	12.7	687	2	D57713	chloride channel C
33	530	12.7	687	2	C57713	chloride channel C
34	519.5	12.4	871	2	AC2417	hypothetical prote
35	504.5	12.1	687	2	B57713	chloride channel K
36	481.5	11.5	686	2	A45483	chloride channel,
37	459	11.0	899	2	S76449	hypothetical prote
38	371.5	8.9	792	2	A84308	chloride channel l
39	370.5	8.9	512	2	H86832	hypothetical prote
40	342.5	8.2	468	2	C82449	conserved hypothet
41	336	8.0	521	2	A95134	voltage-gated chlo
42	336	8.0	521	2	E98002	conserved hypothet
43	314	7.5	586	2	A12065	hypothetical prote
44	304.5	7.3	473	2	AE0527	probable membrane
45	304.5	7.3	589	2	F69426	chloride channel,

## ALIGNMENTS

## RESULT 1

I37240

N:Contains: chloride channel protein 3, long form - human

C:Species: Homo sapiens (man)

C&gt;Date: 24-May-1996 #sequence, revision 24-May-1996 #text\_change 21-Jul-2000

C/Accession: I37240; I37241; S55475

R/Borsani, G.; Ruggeri, E.T.; Tagliatela, M.; Wong, C.; Ballabio, A.

Genomics 27, 131-141, 1995

A&gt;Title: Characterization of a human and murine gene (CLCN3) sharing similarities to

A/Reference number: A57067; M01D:95394449; PMID:7665160

A/Accession: I37240

A&gt;Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 1-820 &lt;RES&gt;

A/Cross-references: EMBL:X78520; NID:g854101; PIDN:CAA55280.1; PID:g854102

A/Accession: I37241

A&gt;Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: mRNA

A/Residues: 59-820 &lt;RES&gt;

A/Cross-references: EMBL:X78520; NID:g854101; PIDN:CAA55281.1; PID:g854103

C/Genetics:

A/Gene: GDB:CLCN3

A/Cross-references: GDB:270665; OMIM:600580

A/Map position: 4pter-4qter

Query Match 96.4%; Score 4026; DB 2; Length 820;  
Best Local Similarity 96.9%; Pred. No. 2,8e-308;

Matches 776; Conservative 1; Mismatches 10; Indels 14; Gaps 4;

QY	3	ASSDPYLPYDGG-----DNIPRLRLKRGHYTYTNGSINSSTHLLDLDEPT 52	
DB	22	ASSDEEL-LDGAIVINDFOQTSDDNL-LDGDYAVGHYTYTNGSINSSTHLLDLDEPT 79	
QY	53	PGVGYDDDFHTIMVREKCKDRHRIRNSKKESAWEMTKSLYDASGLVYTLGLAS 112	
DB	80	PGVGYDDDFHTIMVREKCKDRHRIRNSKKESAWEMTKSLYDASGLVYTLGLAS 139	
QY	113	GALAGLIDIAADMTDKESICISALWYNHQQCWGNSNETTFEERDKCPQWKTAELIIG 172	
DB	140	GALAGLIDIAADMTDKESICISALWYNHQQCWGNSNETTFEERDKCPQWKTAELIIG 199	
QY	173	QAQPGSYIMNYIMYFWALSFAPLAVSLVAPACGSGEIPETITISGFTIRGLCK 232	
DB	200	QAQPGSYIMNYIMYFWALSFAPLAVSLVAPACGSGEIPETITISGFTIRGLCK 259	
QY	233	WTLMKITITLVAVASGLSGKEGPLVHVACCGGNTFSYLFPPYSTNEAKKREVLASA 292	
DB	260	WTLMKITITLVAVASGLSGKEGPLVHVACCGGNTFSYLFPPYSTNEAKKREVLASA 319	
QY	293	AGVSVAFGAIGVLFSLLEVSYTFPLKTLWRSPFALVAAPVLRISINPGNSRLVLPY 352	

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Db 320 AGSVAGAPIGVLFLEEVSYYPELKTLMRSFPAALVAAFLRSINPFGNSRLVLEYV 379
QY 353 EYHFWLFELEPFLILGVFGGLWGAFFIRANIAMCRKRSTKFGKPVLEVIIVAAITA 412
Db 380 EYHFWLFELEPFLILGVFGGLWGAFFIRANIAMCRKRSTKFGKPVLEVIIVAAITA 439
QY 413 VIAFPNPTRLNTSELKELFTDCGPLESSSLCDYRDMNASKIVDDIPDRPAGIGYSA 472
Db 440 VIAFPNPTRLNTSELKELFTDCGPLESSSLCDYRDMNASKIVDDIPDRPAGIGYSA 499
QY 473 IMWLCLALFEIIMTVTFPGIKVPSGLFIPSMALGATAGRVGAVGQALYYHHDFLEK 532
Db 500 IMWLCLALFEIIMTVTFPGIKVPSGLFIPSMALGATAGRVGAVGQALYYHHDFLEK 559
QY 533 EMCVAGADCTIPGLYAAVGAACGGVTRMTVSLVIVFELTGLLEYIVPLMAAVMTSKW 592
Db 560 EMCVAGADCTIPGLYAAVGAACGGVTRMTVSLVIVFELTGLLEYIVPLMAAVMTSKW 619
QY 593 VGDAFREGIYEAHIRLNGYRPFELDAKE--EFTHTTLADAVMRPRNDPPLAVLTQDNMTV 650
Db 620 VGDAFREGIYEAHIRLNGYRPFELDAKEEFTHTTLADAVMRPRNDPPLAVLTQDNMTV 679
QY 651 DDIEINMINSYNGFPVIMSKESQRLVGFALRDLTIAIESARKKQGIYSSVRCFAQH 710
Db 680 DDIEINMINSYNGFPVIMSKESQRLVGFALRDLTIAIESARKKQGIYSSVRCFAQH 739
QY 711 TPSPASPRLKLRSLIDMSPTVTDHTPMEIYVDIFRKLGRLQCLVTHNGRLLGITTK 770
Db 740 TPSPASPRLKLRSLIDMSPTVTDHTPMEIYVDIFRKLGRLQCLVTHNGRLLGITTK 799
QY 771 KDILRHMAQTANODPASIMFN 791
Db 800 KDILRHMAQTANODPASIMFN 820

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## RESULT 2

chloride channel 3 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Nov-1999  
 C:Accession: I48295; S53473  
 R:Borsani, G.; Ruggeri, E.I.; Tagliatalela, M.; Wong, C.; Ballabio, A.  
 A:Title: Characterization of a human and murine gene (CLCN3) sharing similarities to vol  
 A:Reference number: A57067; MUID:95394449; PMID:7665160  
 A:Accession: I48295  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-760 <RES>  
 A:Cross-references: EMBL:X78874; NID:9854275; PIDN:CAA55476.1; PID:9854276  
 C:Genetics:  
 A:Gene: CLCN3

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Query Match 95.7%; Score 3996; DB 2; Length 760;
Best Local Similarity 99.7%; Pred. No. 5,7e-306;
Matches 756; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 32 MTNGSINSHLLDLDLDEPIPGVGYDDFHTIDMREKCKDRRHRIRINSKKESAMEM 91
Db 1 MTNGSINSHLLDLDLDEPIPGVGYDDFHTIDMREKCKDRRHRIRINSKKESAMEM 60
QY 92 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMMDLKREGICLSALMYNHQCCWGSNE 151
Db 61 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMMDLKREGICLSALMYNHQCCWGSNE 120
QY 152 TTFEERKCKPQWKMAELIIGQAGPGSYIMNYIMYFMALSFAPLAVSLVKYFAPYACG 211
Db 121 TTFEERKCKPQWKMAELIIGQAGPGSYIMNYIMYFMALSFAPLAVSLVKYFAPYACG 180
QY 212 SGPEIRTIISGFIIRGYLCKWMLMTITTLVLAVASGLSGKRGPLVHVAACCGGINFSY 271
Db 181 SGPEIRTIISGFIIRGYLCKWMLMTITTLVLAVASGLSGKRGPLVHVAACCGGINFSY 240

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QY 272 LFPKYSTNEAKKREVLASAASAGVVAFGAPIGGVLFLEEVSYYPELKTLMRSFPAALV 331
Db 241 LFPKYSTNEAKKREVLASAASAGVVAFGAPIGGVLFLEEVSYYPELKTLMRSFPAALV 300
QY 332 AAFVLRSTINPFGNSRLVLFVEYHITPWLPELLPFLILGVFGGLWGAFFIRANIAMCRRR 391
Db 301 AAFVLRSTINPFGNSRLVLFVEYHITPWLPELLPFLILGVFGGLWGAFFIRANIAMCRRR 360
QY 392 KSTFGKYPVLEVIIVAAVAVIAFNPYTRLNTSELKELFTDCGPLESSSLCDYRDM 451
Db 361 KSTFGKYPVLEVIIVAAVAVIAFNPYTRLNTSELKELFTDCGPLESSSLCDYRDM 420
QY 452 NASKIVDDIPDRPAGIGYSAIMQLALFEIIMTVTFPGIKVPSGLFIPSMALGATAG 511
Db 421 NASKIVDDIPDRPAGIGYSAIMQLALFEIIMTVTFPGIKVPSGLFIPSMALGATAG 480
QY 512 RIVGIAVQOLAYYHHDFIFREKCEVGADCTPGLYAAVGAACGGVTRMTVSLVIVF 571
Db 481 RIVGIAVQOLAYYHHDFIFREKCEVGADCTPGLYAAVGAACGGVTRMTVSLVIVF 540
QY 572 ELTGLLEYIVPLMAAVMTSKWVGDAFREGIYEAHIRLNGYRPFELDAKEEFTHTTLADVM 631
Db 541 ELTGLLEYIVPLMAAVMTSKWVGDAFREGIYEAHIRLNGYRPFELDAKEEFTHTTLADVM 600
QY 632 RPRNDPPLAVLTQDNMTVDDIENMINETSYNGFPVIMSKESQRLVGFALRDLTIAIES 691
Db 601 RPRNDPPLAVLTQDNMTVDDIENMINETSYNGFPVIMSKESQRLVGFALRDLTIAIES 660
QY 692 ARKQEGIVGSSRVCFAQHPTPSLPAESPRPLKLSIIDMSPTVTDHTPMEIYVDIFRKL 751
Db 661 ARKQEGIVGSSRVCFAQHPTPSLPAESPRPLKLSIIDMSPTVTDHTPMEIYVDIFRKL 720
QY 752 GLRQCLVTHNGRLLGITTKKDILRHMAQTANODPASIMFN 791
Db 721 GLRQCLVTHNGRLLGITTKKDILRHMAQTANODPASIMFN 760

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## RESULT 3

protein kinase C-regulated chloride channel - black rat  
 C:Species: Rattus rattus (black rat, roof rat)  
 C>Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I58159  
 R:Kawasaki, M.; Uchida, S.; Monkawa, T.; Miyawaki, A.; Mikoshiba, K.; Marumo, F.; Sas  
 Neuron 12, 597-604, 1994  
 A:Title: Cloning and expression of a protein kinase C-regulated chloride channel abun  
 A:Reference number: I58159; MUID:94206538; PMID:8155321  
 A:Accession: I58159  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-760 <RES>  
 A:Cross-references: GB:D17521; NID:9473727; PIDN:BA04471.1; PID:9699624  
 C:Genetics:  
 A:Gene: CLC-3

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Query Match 95.6%; Score 3994; DB 2; Length 760;
Best Local Similarity 99.5%; Pred. No. 8,2e-306;
Matches 756; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 32 MTNGSINSHLLDLDLDEPIPGVGYDDFHTIDMREKCKDRRHRIRINSKKESAMEM 91
Db 1 MTNGSINSHLLDLDLDEPIPGVGYDDFHTIDMREKCKDRRHRIRINSKKESAMEM 60
QY 92 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMMDLKREGICLSALMYNHQCCWGSNE 151
Db 61 TKSLYDAMSGMLVVTTLTGLASGALAGLIDIAADMMDLKREGICLSALMYNHQCCWGSNE 120
QY 152 TTFEERKCKPQWKMAELIIGQAGPGSYIMNYIMYFMALSFAPLAVSLVKYFAPYACG 211
Db 121 TTFEERKCKPQWKMAELIIGQAGPGSYIMNYIMYFMALSFAPLAVSLVKYFAPYACG 180
QY 212 SGPEIRTIISGFIIRGYLCKWMLMTITTLVLAVASGLSGKRGPLVHVAACCGGINFSY 271
Db 181 SGPEIRTIISGFIIRGYLCKWMLMTITTLVLAVASGLSGKRGPLVHVAACCGGINFSY 240

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Db 181 SGPEIKTILSGFIRNGYLCKMTLMKTTTLVLAVASGLSGKEGRLVHVHACCGNIFSY 240  
 QY 272 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSELEVSYPPLKTLMSFEALV 331  
 Db 241 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSELEVSYPPLKTLMSFEALV 300  
 QY 332 AAVLVASINFGNSRLVLFVEVHTPWYLELPPFILLGVFGGLMGAFIRANIAMCRR 391  
 Db 301 AAVLVASINFGNSRLVLFVEVHTPWYLELPPFILLGVFGGLMGAFIRANIAMCRR 360  
 QY 392 KSTKFGKYPVLEVIYAALTAVALAFPMPTRLNLSLTKELFTDCGLSESSLCDYRNDM 451  
 Db 361 KSTKFGKYPVLEVIYAALTAVALAFPMPTRLNLSLTKELFTDCGLSESSLCDYRNDM 420  
 QY 452 MASKIVDDIPDRPAGIGVSAIMOLCLALFKITMTVFTFGIKVPSGLFIPSAIGAIA 511  
 Db 421 MASKIVDDIPDRPAGIGVSAIMOLCLALFKITMTVFTFGIKVPSGLFIPSAIGAIA 480  
 QY 512 RIYGIAGEOLATYHHDMFTIKENCVEGADCTPGLIYAMGAAACLGVTMTVSLVIVF 571  
 Db 481 RIYGIAGEOLATYHHDMFTIKENCVEGADCTPGLIYAMGAAACLGVTMTVSLVIVF 540  
 QY 572 ELTGGLLEYIVPLMAAVMTSKWGDAGREGIYEAHTRLNGLYPLDAKEEFTHTTLADVM 631  
 Db 541 ELTGGLLEYIVPLMAAVMTSKWGDAGREGIYEAHTRLNGLYPLDAKEEFTHTTLADVM 600  
 QY 632 RPRRNDPPLAVLTQDNMTVDDIENMTINETSNGFPYIMSKESQRLVGFALRDLTLAIES 691  
 Db 601 RPRRNDPPLAVLTQDNMTVDDIENMTINETSNGFPYIMSKESQRLVGFALRDLTLAIES 660  
 QY 692 ARKKOGIYSSSVCAQHTPSPAPSPRLKRLSLDMSPFVTVDHTPMEIVVDIFRKL 751  
 Db 661 ARKKOGIYSSSVCAQHTPSPAPSPRLKRLSLDMSPFVTVDHTPMEIVVDIFRKL 720  
 QY 752 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 791  
 Db 721 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 760

## RESULT 4

137242  
 chloride channel - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence-revision 29-May-1998 #text-change 21-Jul-2000  
 C:Accession: I37242  
 R:van Slegtenhorst, M.A.; Bassil, M.T.; Borsani, G.; Wapenaar, M.C.; Ferrero, G.B.; de CC  
 Hum. Mol. Genet. 3, 547-552, 1994  
 A:Title: A gene from the Xp22.3 region shares homology with voltage-gated chloride chan  
 A:Reference number: I37242; M0ID:94348498; PMID:8069296  
 A:Accession: I37242  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-760 <RES>  
 A:Cross-references: EMBL:X77197; NID:g479158; PIDN:CA54417.1; PID:g479159  
 C:Genetics:  
 A:Status: preliminary  
 A:Gene: GDB:CLCN4  
 A:Cross-references: GDB:270666; OMIM:302910  
 A:Map position: Xp22.3-Xp22.3

Query Match 78.4%; Score 3273; DB 2; Length 760;  
 Best Local Similarity 77.9%; Pred. No. 4, 1e-249;  
 Matches 592; Conservative 83; Mismatches 85; Indels 0; Gaps 0;  
 QY 32 MTNGGSINSTHLLDLDEPIPGVGYDFHTIDWVREKCKDERHRRIRNSKKESAWEM 91  
 Db 1 MVAAGAMSGSGLMDPLDEPFVGYEDFHTIDWVREKSRQDRIRKRTTSKESIEWE 60  
 QY 92 TKSLYAMSGWLVVTLTGASGALAGLIDTADWMTDLKEGICLSALWYNHQCQGSNE 151  
 Db 61 IKSLYAMSGWLVVTLTGAGTLAGVLDLAVWMTDLKEGVCLSAFWYSHEQCQWTSN 120  
 QY 152 TTEEDRDKCPQWKTWELLIIQGAEGSGYIMNYIMTIFNALSFAPLAVSLVYKFAFYAG 211

Db 121 TTEEDRDKCPQWKTWELLIIQGAEGSGYIMNYIMTIFNALSFAPLAVSLVYKFAFYAG 180  
 QY 212 SGPEIKTILSGFIRNGYLCKMTLMKTTTLVLAVASGLSGKEGRLVHVHACCGNIFSY 271  
 Db 181 SGPEIKTILSGFIRNGYLCKMTLMKTTTLVLAVASGLSGKEGRLVHVHACCGNIFSY 240  
 QY 272 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSELEVSYPPLKTLMSFEALV 331  
 Db 241 LFPKYSTNEAKKREVLISAASAGVSAFAPIGVLFSELEVSYPPLKTLMSFEALV 300  
 QY 332 AAVLVASINFGNSRLVLFVEVHTPWYLELPPFILLGVFGGLMGAFIRANIAMCRR 391  
 Db 301 AAVLVASINFGNSRLVLFVEVHTPWYLELPPFILLGVFGGLMGAFIRANIAMCRR 360  
 QY 392 KSTKFGKYPVLEVIYAALTAVALAFPMPTRLNLSLTKELFTDCGLSESSLCDYRNDM 451  
 Db 361 KSTKFGKYPVLEVIYAALTAVALAFPMPTRLNLSLTKELFTDCGLSESSLCDYRNDM 420  
 QY 452 MASKIVDDIPDRPAGIGVSAIMOLCLALFKITMTVFTFGIKVPSGLFIPSAIGAIA 511  
 Db 421 MASKIVDDIPDRPAGIGVSAIMOLCLALFKITMTVFTFGIKVPSGLFIPSAIGAIA 480  
 QY 512 RIYGIAGEOLATYHHDMFTIKENCVEGADCTPGLIYAMGAAACLGVTMTVSLVIVF 571  
 Db 481 RIYGIAGEOLATYHHDMFTIKENCVEGADCTPGLIYAMGAAACLGVTMTVSLVIVF 540  
 QY 572 ELTGGLLEYIVPLMAAVMTSKWGDAGREGIYEAHTRLNGLYPLDAKEEFTHTTLADVM 631  
 Db 541 ELTGGLLEYIVPLMAAVMTSKWGDAGREGIYEAHTRLNGLYPLDAKEEFTHTTLADVM 600  
 QY 632 RPRRNDPPLAVLTQDNMTVDDIENMTINETSNGFPYIMSKESQRLVGFALRDLTLAIES 691  
 Db 601 RPRRNDPPLAVLTQDNMTVDDIENMTINETSNGFPYIMSKESQRLVGFALRDLTLAIES 660  
 QY 692 ARKKOGIYSSSVCAQHTPSPAPSPRLKRLSLDMSPFVTVDHTPMEIVVDIFRKL 751  
 Db 661 ARKKOGIYSSSVCAQHTPSPAPSPRLKRLSLDMSPFVTVDHTPMEIVVDIFRKL 720  
 QY 752 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 791  
 Db 721 GLRQCLVTHNGRLGIIITKKDILRHMAQTANODPASIMFN 760

## RESULT 5

S47327  
 chloride channel protein 3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change 05-Nov-1999  
 C:Accession: S47327  
 R:Schwappach, B.; Jentsch, T.J.  
 submitted to the EMBL Data Library, September 1994  
 A:Reference number: S47327  
 A:Accession: S47327  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-747 <SCH>  
 A:Cross-references: EMBL:Z36944; NID:g535931; PIDN:CA85406.1; PID:g535932

Query Match 77.6%; Score 3240; DB 2; Length 747;  
 Best Local Similarity 78.4%; Pred. No. 1, 6e-246;  
 Matches 586; Conservative 81; Mismatches 80; Indels 0; Gaps 0;  
 QY 45 LDLDDEPIPGVGYDDFHTIDWVREKCKDERHRRIRNSKKESAWEMTSLYAMSGWLV 104  
 Db 1 MDLDEPFVPGVGYEDFHTIDWVREKSRQDRIRKRTTSKESIEWEIKSLDAMSGWV 60  
 QY 105 VTLTGASGALAGLIDTADWMTDLKEGICLSALWYNHQCQGSNETTEEDRDKCPQW 164  
 Db 61 MLTIGLAGTLAGVLDLAVWMTDLKEGVCLSAFWYSHEQCQWTSNETTEEDRDKCPQW 120  
 QY 165 TWAEELIIQGAEGSGYIMNYIMTIFNALSFAPLAVSLVYKFAFYAGSGGIPETKILSG 224  
 Db 121 KWSLELLSQSEGASAVILNLTMIALLFAFLAVSLVYKFAFYAGSGGIPETKILSG 180

OY	225	IRGLGKMTLTKITITVTLAAVSGSLGKEEPLVHVAOCCCNIESYFEPKSTNEAKR	284
Db	181	IIRGLGKMTLTKITVTLVLYVSSGLSKKEEPLVHVAOCCCNIESSLPFSKYSKNEGR	240
OY	285	EVLASAASAAGVAVFAGPAGIGVLFSLSEVSYFPLKTIIMRSEFAALVAFLRSINPEGN	344
Db	241	EVLASAAGVAVFAGPAGIGVLFSLSEVSYFPLKTIIMRSEFAALVAFLRSINPEGN	300
OY	345	SKLVLFYEVYHPWMLFELFPELILGVFGGLMGAFIRANIANCRRRSTKRGKPVLEV	404
Db	301	SKLVLFYEVYHPWMAELFEPILLGVFGGLMGVFTTCNIAWCRRRKTRIGKPVLEV	360
OY	405	IIVAAITVAVAPNPYTRNLNTSELKELEFTDQCPLESSLCDYRNDNMASKIYVDIDPRP	464
Db	361	IYVTAITAIAPNPYTRNSTSELSELSEFNDCGALESSLCDYINDPMKTRVYDIDPRP	420
OY	465	AGIGVYSAIWOLCLALFKIIMTVFTFCGIKVPSSLFDSMAIGALAGRIVIGIAVEQLAY	524
Db	421	AGVGVYVAMTMOALALIFKIVITVITFTFGMKIPSGLFIPSMAGAMAGRWVIGVQLAYH	480
OY	525	HHDMFIEFKMCEVAGDCTIPGLYAMVGAACLGVTTRTVSLVYVFEELTGLEIYVPLM	584
Db	481	HHDMFIEFRMCPGADCVTPGLYAMVGAACLGVTTRTVSLVYVMEFELTGLEIYVPLM	540
OY	585	AAVMTSKWVGDAFGREGIYEAHIRLNGVPFLDPAKEEFHTTTLAADVMPRRRNDPLAVLT	644
Db	541	AAAVSKWVADAFGREGIYEAHIRLNGVPFLDPAKEEFHTTRITATDVMPPRRRNDPLAVLT	600
OY	645	QDNMTVDIDENMINETSTNGFPVYMSKESQRLVGFALRRDLTIAESARKKOEGIVGSSR	704
Db	601	QDSMTVEVETLIKETDYNQFPVYVSRDSERLIGFAQRRELLAIKNAOROREGIVSNSI	660
OY	705	VCFACHTPSLPESPRLKRSIILMSPEFTVADHPMEIYVDIFPKLGRCLVTHNRL	764
Db	661	MYTFEEPELPANSHPLKRLRILNLSPFTYTDHPIMETVYDIFPKLGRCLVTRGRL	720
OY	765	LGITFKDILRHMAQTANODPASIMFN	791
Db	721	LGITFKDVLRRHMAQMANODPESITFN	747
RESULT 6			
	148294	gene Clcn4 protein - mouse	
		C:Species: Mus musculus (house mouse)	
		C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_Change 05-Nov-1999	
		C:Accession: I48294	
		R:Rugairi, E.I.; Adler, D.A.; Borsani, G.; Tsuchiya, K.; Franco, B.; Hauge, X.; Distchech	
		Nature Genet. 10, 466-471, 1995	
		A:Title: Different chromosomal localization of the Clcn4 gene in Mus spretus and C57BL/6	
		A:Reference number: I48294; MUID:95400329; PMID:7670496	
		A:Accession: I48294	
		A:Status: preliminary; translated from GB/EMBL/DBJ	
		A:Molecule type: mRNA	
		A:Residues: 1-747 <RES>	
		A:Cross-references: EMBL:Z49916; NID:9929679; PIDN:CA990150.1; PID:9929680	
		C:Genetics:	
		A:Gene: Clcn4	
		Query Match 77.0%; Score 3217; DB 2; Length 747;	
		Best Local Similarity 77.6%; Pred. No. Ie-244;	
		Matches 580; Conservative 83; Mismatches 84; Indels 0; Gaps 0;	
OY	45	LDLLEPIPGVGYTDYDFTIDMVREKCKDRERHRRINSKKKESAMEMTKSLDYAMSGGLY	104
Db	1	MDLLEPPDVGTEIDFHTIDMLREKSRDIDRHKRTSKSESTIWEPIKSLDYAMSGWV	60
OY	105	VLTUIGASGALAGLIDIAADWMTDLKEGICLSALVYNHEOCWCMSNETTFEERDKCPOMK	164
Db	61	MLLIGLLAGTAGVIDLAVDMWMTDLKEGVCLSAFVYSHQCCWTSNETTFEDRDKCPIMQ	120
OY	165	TWAEILIQDAQBGSGYIMNYIMYIFWALSPAFVAVLVKVPAPACGSGGIDPIKTIISGF	224

Db	121	KSESSLSQSEGSASVYIINLYMILMALFLPFLASLVRVFAVYACGSGIPEIKTILSGF	180
Qy	225	IRGLGKWTLMIKRTITVLAVASGLSLGKBGPLVHVAOCCGNIFSYLPPRYSTNEAKKR	284
Db	181	IRGLGKWTLLIKRTITVLAVVSSGLSGKBGPLVHVAOCCGNIFSYLPSYKKEGKR	240
Qy	285	EVLASAASAGSVAFAGAPIGVLFSLIEEYSYFPLKTLMRSPFAALVAFLRSINPGN	344
Db	241	EVLASAAAGSVAFAGAPIGVLFSLIEEYSYFPLKTLMRSPFRALVAFLRSINPGN	300
Qy	345	SLVLVFEYEHHPWLFELFPLILLGVFGGLMGAFITANIAMCKRRKSTYRGKPVLEV	404
Db	301	SLVLVFEYEHHPWMAELFPLILLGVFGGLMGLFTFCNIAWCRKRRKTYRLGRPVLEV	360
Qy	405	IIVAAITVIAFPNPYTRLNTSELKELFTPOGPLESSLCDYRNDMAKSIVDIDPDR	464
Db	361	IAVTAVTAVIAFPNPYTRQSTSELSELFPCNOGALESSQLCDYINDPMKTRPVDDIDPR	420
Qy	465	AGIGVYSALIMOLCLALFKRIIMVFTEGIKVPSGLFIPSMALGALAGIIVGLIAVEQLAVY	524
Db	421	AGVGYVTMMQDLALVLEFKYITVITFTPMKIPSGLFIPSMAGVAMAGMVIGIVEQLAVH	480
Qy	525	HHDMWIFRMEKCEVGADCTIPGLYAMVGAACIGVTRMTVSLVYVLPFLTGGLEYIVLM	584
Db	481	HHDMWIFRMCPRGADCVTPGLYAMVGAACIGVTRMTVSLVYIMFLTGGLEYIVLM	540
Qy	585	AAVMTSKWVGDAFGREGIYEAHRIRLNGYFLDAAKEEFTHTTLAADVMRRRNDPPLAVLT	644
Db	541	AAAVTSKWVAADFEGEYIEAHRIIRLNGYFLDVKKEFHTRLATDVMRRRNDPPLAVLT	600
Qy	645	ODNMVVDIEENNINETSNGFPVIMSKESORVGLPDRDLTIAESARKROEGIVGSSR	704
Db	601	ODSMVVEDEVEILIKTDYNGFPLVLSRDSERLIGFAQRRELLAIKNAKROEGIVSNI	660
Qy	705	VCFACHTPSLPAESRPRLKRSILDMSPFTYDHTPMEIIVDFIKIGLROCLVTHNGRL	764
Db	661	MYFTEPEPELTPANSPHPLKRLRIFNLSPFTYDHTPMEIVDIFIKIGLROCLVTRSGRL	720
Qy	765	IGIITKKDILIRMAOTANODPASTIMEN	791
Db	721	IGIITKKDYLIRMAOMANODPESTIMEN	747

RESULT 7  
 t19065  
 probable protein kinase C-regulated chloride channel C07H4.2 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: t19065; t25256  
 R:percy.C.  
 submitted to the EMBL Data Library, January 1996  
 A:Reference number: z19068  
 A:Accession: t19065  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-735 <WIL>  
 A:Cross-references: EMBL:Z66334; PIDN:CAA92728.1; GSPDB:GN00020; CESP:C07H4.2  
 A:Experimental source: clone C07H4  
 R:Lightning, J.  
 submitted to the EMBL Data Library, September 1995  
 A:Reference number: Z20005  
 A:Accession: t25256  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-735 <WT2>  
 A:Cross-references: EMBL:Z54216; PIDN:CAA90949.1; GSPDB:GN00020; CESP:C07H4.2  
 A:Experimental source: clone T24H10  
 C:Genetics:  
 A:Gene: CESP:C07H4.2  
 A:Map position: 2  
 A:Introns: 35/2; 81/3; 242/3; 297/3; 337/2; 537/3; 634/2; 682/3



Qy	328	AALVAAPVLINSINFGSRLVLEYVEHPPMYLEFEPFLLIGVGGLMAFEIPRANITAM	387
Db	304	CGVAVLAIQSSVDMITMGRIVQFSVNTQHNMFELPMFAIGCTGCGMGSTFSVNLHV	363
Qy	388	CRRRKSTKFGKPYLEVIIVAATTAIVIAFPNPYTRINTSELIKELFTDGPBLESSLCDY	447
Db	364	GRWRKK-HLRQMRIVEVAVAATGVVNFLETPYGGSMLELGDFOCTPCTPGTMEKE-	421
Qy	448	RNDMAKSIYDDIDFDRAGAGVVSALMQLALIEFIINTVTFTEGIKVPSGLFIPTSMIG	507
Db	422	DSDLR-----AFSLLVTAATAFAAFATVGTGFPAGILVPSLTIG	462
Qy	508	AIAGRIGIAVEOLAYYHHMFTEFKEMCEYAGDCIRPGLYAAGAACIGVTRMTVSLV	567
Db	463	ALYGRACGMFRALQIEYVASSYIFTE-CYDDQDCVAPGVYALVGAAMLTGVTHTMTCILA	521
Qy	568	VIVFELTGLEGLEYVPLMAAVMTSKWWDAGFREGIYEAHIRLNGVYFELDAKEEPTHTTLA	627
Db	522	IIMFELTSGLEWYVPVIVIGILCAKAGAEVAGVGTGEIIEENKRLPYDLPKKEFLDEVA	581
Qy	628	ADVWRPPRPDPLAVLVLQDMWTVDLIENNINENSYNGFVIVIKSESQRJYRGALRBDITI	687
Db	582	KDXY-----GNKQFVLTAIVGLQVRDINELVTKNNTGFPVYESLSDVYLLGLTAPPKVYR	637
Qy	688	AIESARRKQEGIVSSSFVCEAQTPSLPAESP-RPLKRSILDMSPFVYTDHTPMEIYVD	746
Db	638	ALQVAAARNSDMNINITYIRE-KTKPSHSRDATFLEVDLIGLIESCLLQVEPECVSKITLY	696
Qy	747	IERTLGRQCLYTHNGRLGLIITKKDILRRM	777
Db	637	LEKSLGTHHHTFVCYSKEGFPISKDDINFM	727

hypothetical protein SPBC19C7.11 - fission yeast (*Schizosaccharomyces pombe*)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_reviseion 03-Dec-1999 #text\_change 03-Dec-1999  
C:Accession: T39817  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gallardín, C.  
submitted to the EMBL Data Library, June 1998  
A:Reference number: Z21881  
A:Accession: T39817  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-812 <LYN>  
A:Cross-references: EMBL:AL023859; PIDN:CA19579.1; GSPDB:GM00067; SPDB:SPBC19C7.11  
A:Experimental source: strain 972h-; cosmid c19C7  
C:Genetics:  
A:Gene: SPDB:SPBC19C7.11  
.:Map position: 2

Query Match	24.3%	Score 1015	DB 2	Length 812
Best Local Similarity	32.0%	Pred. No. 1.6e-71		
Matches 240	Conservative 142	Mismatches 275	Indels 94	Gaps 17

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0Y      72 KDREHRRINSKKK-----SAMEKTSLYDAMGWLVTITGLASALGLIDIAADM 126
Db      64 KDRV-NELINEONEENNVNIDOSRMSKMRIMWVGISWFLISITIGTVFAAMMEDIYISWL 1222
0Y      127 TDLKEGICLSALWYNHEOCMG-----NETTFEERDKCPOMKWTABELIGQAE 1797
Db      123 SDIRRGYCTSHMYNYNEKRCOCWYSEMGCFKHDLYNDLFE-QGSSCTFAMKPMTY----- 1744
0Y      176 GPGSTINMYIMFWALSFAPLAVSLVKVPAPYACGSIPEIKTILSGFIIRGLGKWTL 2355
Db      175 ---KFSLENYLITAFALFEVCAAIWADVAPLAAAGSISEIKCIIIGFLDFSPLSFRVM 2313
0Y      236 MIKTTTLVLAASGISGKEBGLVHVAVCCCNIFISYLFPPKSTNEAKKREVLASAASAGV 2959
Db      232 LVKCGGLPLAASISGVSKESPVSHLATITGHNSIKFVKYAREGSIIRROICVASAASGV 2911

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OY      296 SVAPCAPJGVLFSLE-----EVSYPELTKLRSPFPAALVAALVFRSINPE 342
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      292 AVAROSPJGVLFEGVEVKFIIEILNFKEMSGCDPRKMIYSPFCCLSAAGVHMLNPF 351
OY      343 GNSRLVLEYVEYHRPWLYLELPPELLCGVGCGLMGAFPIRANIAMCRRRSKTFKGYPVL 402
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      352 RTGGVLEFEVRYSCGMHFELLFCFLGIFGGLGFEFYMRLEPFIOLRKX-YLSRVGL 410
OY      403 EVIIYAATTAVIAPNPVTRINTSELIKELTPDGPLESSS-----LCQVRNDMNSKI 456
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      411 DAAYVTYTTSLVSELINPRLDMTLGNHELLOEC---KSSSPRELINLD----- 457
OY      457 VDDIPDRPAGIGVYSALWQLCALIFKTIIMTVFTFGIKPSGLEIPSMAGIAGRIVGI 516
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      458 -----PSLRKTNTI-LLLIATFPARTIEVFYSKAQVPAGIVEPMSAAGASGYMIGL 508
OY      517 AVEOLAAYHHMFIFKEKCEVGADCIPTGLAMYGAAACLOGVARMYSLAVIYFELTGG 576
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      509 IAEIMYQRFPMSVLELA-CHGESESCITPGYTAALLGAASLSGINHLVIYIVIMFELIGA 567
OY      577 LEYIPLMAAAMWTSKWVGDAAGREGIYEAHRIKLNGVPEFLDAKEEFFHTTLAADVMRPBRN 636
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      568 INELIPYLVALANLSIGNMLGKITGIADRSEIENGDLPLEBEKSINSNTI-----N 619
OY      637 DPPLAVLTQDNMTYDDIE-----NMINEISYGFPIYMKEEQRLVGFRLRDLTIAI 689
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      620 IPITEVMAASNLTITPISGIFTWRKLLKLGMEGYDESGYPAVDLSRSNYLTLGTAKSSLSSPF 679
OY      690 ESARKKOGSIGSSKVSQAQ-----HTPSPAPESPRLKLRSLIDMSPPVTJTHPMEI 743
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      680 EAA-KLEPSFFPDQDLGCVKDVSDGSKSKSFGESEDR-IDLSAVMDVNPISVLHTQSIAN 737
OY      744 VVDIRKRGLQCLOLVTHNGRLGITTKDIL 774
       :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db      738 VAUFEVLSPVIFLEKDGNLVGLSKDKDL 768

```

RESULT 11

S50054

chloride channel protein CLC-1 - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein GTC779; protein J1616; protein YJ040W; voltage-gated chlo

C:Species: *Saccharomyces cerevisiae*

C:Date: 13-Jan-1995 #sequence\_revision 24-Feb-1995 #text\_change 29-Oct-1999

A:Accession: S50054; S39904; S57059; S63763

R:Huang, M.E.; Chuat, J.C.; Galibert, F.

J. Mol. Biol. 242: 595-598, 1994

A:Title: A voltage-gated chloride channel in the yeast *Saccharomyces cerevisiae*.

A:Reference number: S50054; MUID:95018225; PMID:7932775

A:Accession: S50054

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-779 <HUA>

A:Cross-references: EMBL:L29347; NID:9576927; PIDN:AA53399.1; PID:q576928

R:Greene, J.R.; Brown, N.H.; DiDomenico, B.D.; Kaplan, J.; Eide, D.J.

Mol. Gen. Genet. 241, 542-553, 1993

A:Title: The GCF1 gene of *Saccharomyces cerevisiae* encodes an integral membrane prote

A:Reference number: S39904; MUID:94088447; PMID:7505388

A:Accession: S39904

A:Molecule type: DNA

A:Residues: 1-12, 'R', 14-206, 'L', 208-256, 'T', 258-261, 'L', 263-496, 'I', 498-779 <GRE>

A:Cross-references: EMBL:J23117; NID:9619512; PIDN:CA80663.1; PID:q435339

R:Huang, M.E.; Chuat, J.C.; Galibert, F.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S57052

A:Accession: S57059

A:Molecule type: DNA

A:Residues: 1-779 <MAN>

A:Cross-references: EMBL:Z49540; NID:91015690; PIDN:CA89567.1; PID:q1015691; MIPS:YJ

R:Huang, M.E.; Chuat, J.C.; Galibert, F.

Yeast 11, 775-781, 1995

A:Title: Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes

A:Reference number: S63757; MUID:95397595; PMID:7668047

071 AE-----SUKVGFALNRULI--IAIESAKNDGSLVGSSNVCFAOHTPSLPAESPRKIL / 24  
:: : |: | : | : | : | :  
629 EDKFEKEKRIGYVLKRLHLASKIMQSNSTK---AQTLTVYFNNSNEEL-CHRENCIGF 684

Dd

QY 560 TRMTVSLVIVFELTGLEIYIPVLPMAAVMTSKWVGDAFGREGIYEAHTRLNGYPF  
|||::|| : : : : : : : : : : |||::||| |

Db 558 VRMTISLTAIMKATKDITEGLPIMVLVMWTWKVGDMF-NEGILYDAHDIAEVPFI





[illegible]

RESULT 15  
568428  
Probable chloride channel CLC-6 - human  
C/Species: Homo sapiens (man)  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999  
C/Accession: 568428; S51659  
R:Brandt, S.; Jentsch, T.J.  
FEBS Lett. 377, 15-20, 1995  
A>Title: CLC-6 and CLC-7 are two novel broadly expressed members of the CLC chloride channel family  
A:Reference number: 568426; MUID:96130311; PMID:8543009  
A:Accession: 568428  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-869 <BBR>  
A:Cross-references: EMBL:X83378; NID:q154676; PIDN:CAA58292.1; PID:q1563890

Query Match	Similarity	Score	DB	Length
C:Map position: 1p36				
C:Keywords: chloride channel; glycoprotein; transmembrane protein				
F:81-98/Domain: transmembrane #status predicted <TM1>				
F:126-156/Domain: transmembrane #status predicted <TM2>				
F:179-198/Domain: transmembrane #status predicted <TM3>				
F:241-265/Domain: transmembrane #status predicted <TM4>				
F:280-298/Domain: transmembrane #status predicted <TM5>				
F:344-355/Domain: transmembrane #status predicted <TM7>				
F:371-386/Domain: transmembrane #status predicted <TM8>				
F:462-507/Domain: transmembrane #status predicted <TM9>				
F:521-568/Domain: transmembrane #status predicted <TM11>				
F:410,422/Binding site: carbohydrate (Asn) (covalent) #status predicted				
Query Match	17.48	Score 725.5	DB 2	Length 869
Best Local Similarity	25.38	Pred. No. 1e-48		
Matches 235	Conservative 142	Mismatches 245	Indels 307	Gaps
49	DEIPGVGVGYDPTIDVREKCC	-----KDRERHRRIRSKKESASAMETKSLYD	97	
40	DEILP-----RKDYSLDY	-DRCINDPYLEVLFTMDKKKGRYAVK-----	80	
98	AMSGMLVVTLTGLASLAGLIDIDAMMDLKEGICLSALMTNHEDCCGSMETFEER	157		
81	-----WVVFAIGVCTGVLGVLEDFEVLFTDLKRGVV-----	-----QTSVEE-----	119	
158	DKCPQMKWMAILLIGQAGPESYIMNYIMYFMALSFAPLAVLSLVKFAFAYAGSGSIPET	217		
120	-----CSQ-----	-----KCCALSLLELIGFMTLVFLA-SLTVLITFVYAAAGSGIPEV	162	
218	KTLSGFLIRGVLCRWTLMTITTLVLAVASGLSLGKRGPLVHVACCG-----	266		
163	KCYLNGVAVPQIVRLRTLLCVLSEVLEAVSGLEVGEGPIHSGSVAGAGLPQFQISL	222		
267	NIFSVLPKYSTNKAKKREVLSAASACVSYARCAPIGCVLFSLEEYSYFPLKTLMRSF	326		
223	RKIQNFQ-YYRSPRDKDFEYSAQAAGVAFAFGPILGTLFSEBSSSFMNGLTWKVL	281		
327	FAALVAEVLK-----SINFGGSRLL-VLEVEYVHTP-----	WYFELFEPILLG	370	
282	FCMSMATEPTLNFRRSGIQFGSMGSGFOLPGLLNFGEFCQSDKCHILMTAMDIGFEVVMG	341		
371	VFGGLMGAFETIRANIMCRRKSKTKF-----GKYP-----	VLEVIYVAITAVIAFPPPT	421	
342	VIGGLGATFN-----CLNRKLAKYRMRNVHPKPLVRLLESLLVLTVVVF-----	390		
422	RLNSELKELFETGCGPLESSSLCDYRNDMAKIVDI-----	460		
391	-----VASMYLGECKRQSSSS-----QIGNDSYQLOVTEDEVASSIKTFPCRPDYNDAATLE	442		
461	-----PDRPACI-----GYVSAIMQLCALIFKTIIMTFVFGIKYPSGLFTPSMAIGAIAGR	512		
443	FNPQESALIQLEHODGFTEFSPY-TLALFFVLYFLIACWTYGISVPSGLFVPSLLCGAAGFR	501		
513	IVGLAVBDLAAYYHHDWIFEFKCEKCVGADCTIPGLYAAVVAACAGVTRRTVSLVYVFE	572		
502	LVANLVLS-----	IGGHYISGFEALIGAAAFGGVAMRTISLFTVILIE	546	
573	LTTGLEIVLPMLAAVMTSKWGDAGREGIEAHLIRNGYRPLDAAKEEFHTTL-ADAVM	631		
547	STNELTITGLPIMVTLMAWAKMTGDFNK-GITDIIHGLRGVPLLEMEFEVEMDKLRASDIM	605		
632	RPRRNDPLAVLTODNKT-----	VDDIENMINETSYNGEPVY-----	668	
606	EP-----NLTVVYPHTRISLIVSLRTTYVHAHFAFPVVTENRGNEKEEFMKGNOL	652		
669	-----MSKESRLVGF-----ALRR-----DLTIIAESARKROE-----	697		
653	ISNNIKFRKSSILTRAGEQRRKRSQMSKSYSSSELIRNMCDHIASEEPAEKEDLLOOMLER	712		
698	-----	GIVGSSR-----VCFADHTSPLAESP	719	
713	RYTVPNLYVPOSSSEDMTEERRPLTFHGLIRSLQVLTLVNGVYVSSQSS--ASQP	770		

QY 720 R-----PLKRSILDM-----SPTVTDHPTMEIIVVDIFRKL 751  
 Db 771 RLSTYAEAMADYPRYPDIHDLDTLLINPRMIYDVTPYMNPSPTVSPNTHVSQVFNLFRTM 830  
 QY 752 GLRQC-LYTHNGRLGIIITKKDILRHMAQ 779  
 Db 831 GLRHLPYVNAVGETVGIIITRHNLTYEFLQ 859

Search completed: May 12, 2003, 15:06:01  
 Job time : 54 secs